and second oligonucleotides each independently comprising at least 15 contiguous nucleotides chosen from any of SEQ ID NOs: 1, 2, 3, 4, 20 and 27, or the complement thereof wherein W represents A or T, R represents G or A and Y represents T or C, or a corresponding sequence wherein T has been replaced by U.

39. (new) A polynucleic acid consisting of 10 to 50 nucleotides which specifically hybridizes under conditions allowing discrimination of up to 1 nucleotide mismatch with the sequence of SEQ ID NO:20 wherein Y represents T or C, or with a corresponding sequence wherein T has been replaced by U.

40. (new) A polynucleic acid consisting of 21 to 50 nucleotides which specifically hybridizes with the sequence of SEQ ID NO:20 or the complement thereof wherein Y represents T or C, or with a corresponding sequence wherein T has been replaced by U.

41. (new) A polynucleic acid consisting of 21 to 50 nucleotides which specifically hybridizes under conditions allowing discrimination of up to 1 nucleotide mismatch with the sequence of SEQ ID NO:20 or the complement thereof wherein Y represents T or C, or with a corresponding sequence wherein T has been replaced by U.

42. (new) A polynucleic acid consisting of 27 to 50 nucleotides which specifically

hybridizes under conditions allowing discrimination of up to 1 nucleotide mismatch with the sequence of SEQ ID NO:27 or the complement thereof, or with a corresponding sequence wherein T has been replaced by U.

43. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample by means of a hybridization reaction with a set of oligonucleotides of claims 25 or 38.

44. (new) A method according to claim 43 wherein said oligonucleotides are coupled to a solid support.

45. (new) A method according to claim 28 wherein said polynucleic acids are capture probes.

46. (new) A method according to claim 29 wherein said polynucleic acids are capture probes.

47. (new) A method according to claim 43 wherein said oligonucleotides are capture probes.

48. (new) A method for detecting the presence of an infection with an HCV virus

in a biological sample by means of an amplification reaction using (a set of) primers that specifically hybridize with SEQ ID NO: 1 or SEQ ID NO:3, or the complement thereof wherein W represents A or T, R represents G or A and Y represents T or C; and with SEQ ID NO:20 or SEQ ID NO:27, or the complement thereof wherein Y represents T or C.

49. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample by means of an amplification reaction using (a set of) primers that specifically hybridize with SEQ ID NO:20 or SEQ ID NO:27, or the complement thereof wherein Y represents T or C; and with SEQ ID NO:2 or SEQ ID NO:4, or the complement thereof.

50. (new) A diagnostic kit for the detection of HCV in a biological sample comprising a set of oligonucleotides of claims 25 or 38.

51. (new) A method for the identification of a previously amplified HCV 5' untranslated region fragment comprising hybridizing a set of oligonucleotides of claims 25 or 38 to said 5' region.

52. (new) The process of claim 36 wherein said primer of 15 to 50 nucleotides specifically hybridizing with SEQ ID NO: 1 is combined with a primer hybridizing to the

region extending from nucleotide -68 to nucleotide -1 or the complement of said region.

53. (new) The process of claim 36 wherein said primer of 15 to 50 nucleotides specifically hybridizing with SEQ ID NO:3 is combined with a primer hybridizing to the region extending from nucleotide -68 to nucleotide -1 or the complement of said region.

54. (new) The process according to claim 52 or 53 wherein said primer hybridizing to the region extending from nucleotide -68 to nucleotide -1 or the complement of said region is defined by SEQ ID NO:2 or SEQ ID NO:4.--